

Db 838 GTCCGCTACTTCAGAGAGTGTACTGTGCATGGGAGTCTTAACCATGCTTTTCACTT 779
 Oy 249 CCACGTCATCTCTGCTGGCTCAAAACAGACAGTGTGTCCATTTGACACACAGAGAGT 308
 Db 778 CCACGTCATCTCTGCTGGCTCAAAACAGACAGTGTGTCCATTTGACACACAGAGAGT 719
 Oy 309 GGAATTCGCAAA-----GTATGGCAGCTAGGAAAGACTTCTT 346
 Db 718 GGAATTCGCAAAAGTAATTTACTTGTCTTTCAGTATGGCAGCTAGGAAAGACTTCTT 659
 Oy 347 CCATCAAGCTTAATTTGTTTGTATTCATTTAATTTGACTTCCCTGCTTTACCTAATTA 406
 Db 658 CCATCAAGCTTAATTTGTTTGTATTCATTTAATTTGACTTCCCTGCTTTACCTAATTA 600
 Oy 407 CAAATTTGATGAGTGTGTTTTCCTGCTTTGTTTTCAGTTTGTCTTCTGTAC 466
 Db 599 CAAATTTGATGAGTGTGTTTTCCTGCTTTGTTTTCAGTTTGTCTTCTGTAC 540
 Oy 467 CATATTGTATCTGTGTCAAAATAAGTCCAGTTGGATCTGG 508
 Db 539 CATATTGTATCTGTGTCAAAATAAGTCCAGTTGGATCTGTG 498

 RESULT 3
 AAC03896
 ID AAC03896 standard; cDNA; 482 BP.
 AC AAC03896;
 XX 06-OCT-2000 (first entry)
 DE Human secreted protein 5' EST, SEQ ID NO: 3894.
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 OS Homo sapiens.
 XX EPI033401-A2.
 PN 06-SEP-2000.
 XX 21-FEB-2000; 2000EP-0200610.
 PF 26-FEB-1999; 99US-0122487.
 PR (GEST) GENSET.
 PA Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI: 2000-500381/45.
 DR P-PSDB; AMG03890.
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1: SEQ ID 3894; 71pp + CD-ROM; English.
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 CC well suited for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion

CC vectors.
 SQ Sequence 482 BP; 116 A; 103 C; 121 G; 140 T; 2 other;
 SO Query Match 88.0%; Score 447.2; DB 21; Length 482;
 Best Local Similarity 99.3%; Pred. No. 1.6e-118;
 Matches 457; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

 Oy 2 CCAAAATGGCGGCGACGATGATGTGATACCCGAGCGGCGCAACACAGCGCGGGCA 61
 Db 24 CCAAAATGGCGGCGACGATGATGTGATACCCGAGCGGCGCAACACAGCGCGGGCA 83
 Oy 62 AGAAGCGCTTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 121
 Db 84 AGAAGCGCTTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 143
 Oy 122 TTGATTAAGTGTCCATCTGACAGAACACATTAATGATTTTGCATAGATGTCAAGCTA 181
 Db 144 TTGATTAAGTGTCCATCTGACAGAACACATTAATGATTTTGCATAGATGTCAAGCTA 203
 Oy 182 ACCAGGCGTCCGCTACTGTCAGAAAGTGTGATGTGCATGGGAGTGTGAACCATGCTT 241
 Db 204 ACCAGGCGTCCGCTACTGTCAGAAAGTGTGATGTGCATGGGAGTGTGAACCATGCTT 263
 Oy 242 TTCACCTCCACTGATCTCTGCTGCTCAAAACAGACAGAGTGTGCTCATTGGACACAA 301
 Db 264 TTCACCTCCACTGATCTCTGCTGCTCAAAACAGACAGAGTGTGCTCATTGGACACAA 323
 Oy 302 GAGAGTGGGAATTCCAAAAGTATGGGCACTAGAGAAAGACTTCTTCATCAAGCTTAAT 361
 Db 324 GAGAGTGGGAATTCCAAAAGTATGGGCACTAGAGAAAGACTTCTTCATCAAGCTTAAT 383
 Oy 362 GTTTGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 421
 Db 384 GTTTGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 442
 Oy 422 TGTGTTTTTTCGCTTTGCTTTTTCAGATTTCCTGTTTCT 461
 Db 443 TGTGTTTTTTCGCTTTGCTTTTTCAGATTTCCTGTTTCT 482

 RESULT 4
 AAD12859
 ID AAD12859 standard; cDNA; 3208 BP.
 AC AAD12859;
 XX 16-OCT-2001 (first entry)
 DE Human novel protein (NHP) cDNA with flanking sequences.
 KW Human; novel protein; NHP; protease; gene therapy; aminopeptidase;
 KW obesity; diabetes; high blood pressure; connective tissue disorder;
 KW infertility; infectious disease; antidiabetic; antileukemia;
 KW antibacterial; anorectic; antiviral; ss.
 OS Homo sapiens.
 XX WO200159134-A1.
 PN 16-AUG-2001.
 PD 09-FEB-2001; 2001WO-US04433.
 PF 11-FEB-2000; 2000US-0181924.
 PR (LEXI-) LEXICON GENETICS INC.
 PA Donoho G, Scoville J, Turner CA, Friedrich G, Abulin A;
 PI Zamdrowicz B, Sands AT;
 DR WPI: 2001-488976/53.
 XX

OY 404 TTACAAATTGGATGGAACGTGTGTTTCTGCTTTGTTTTCAGTTTGCATTCTGT 463
 |||||||
 DB 1369 TTACAAATTGGATGGAACGTGTGTTTCTGCTTTGTTTTCAGTTTGCATTCTGT 1428
 |||||||
 OY 464 AGCCATATTGTATTCCTGTGTCAATAAAGTCCAGTTGATTCGG 508
 |||||||
 DB 1429 ACCCATATTGTATTCCTGTGTCAATAAAGTCCAGTTGATTCGG 1473
 |||||||
 RESULT 6
 ID AAA96882 standard; DNA; 327 BP.
 AC AAA96882;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of human ring finger protein ROC1.
 XX
 KM ROC1; ROC2; cullin; ring finger protein; APC1; APC complex; SCF pathway;
 KM cullin dependent ubiquitin ligase; CDK inhibitor; Scl degradation;
 KM tumour; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..327
 FT /tag= a
 FT /product= "ROC1"
 FT
 PN WO200058472-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08592.
 XX
 PR 31-MAR-1999; 99US-0127261.
 PR 22-NOV-1999; 99US-0166927.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Xiong Y, Ohta T;
 DR MPI: 2000-647235/62.
 DR P-PSDB: AAB19160.
 XX
 PT Novel nucleic acid encoding cullin regulating ring finger proteins,
 PT termed as ROC proteins similar to anaphase-promoting complex 11, for
 PT therapeutic and diagnostic use
 XX
 PS Claim 1; Fig 2A; 83pp: English.
 XX
 SQ The present sequence encodes a human ROC1 ring finger protein. The
 CC specification also describes human ROC2. ROC1 and ROC2 are similar
 CC to APC1, a subunit of the APC complex. The proteins stimulate cullin
 CC dependent ubiquitin ligase activity. ROC1 functions in vivo as an
 CC essential regulator of CDK inhibitor Scl degradation by the SCF
 CC (undefined) pathway. ROC proteins are useful for screening bioactive
 CC agents that interfere with the binding of ROC proteins with cullin
 CC proteins. Pharmaceutical formulations comprising ROC proteins are
 CC useful for diagnostic and therapeutic purposes, preferably for
 CC diagnosing and treating tumours.
 CC
 Query Match 64.4%; Score 327; DB 21; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.8e-84;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 ATGGCGGACGATGATGTGATACCCGAGGCGACACAGCGCGGCGGCAAGAG 66
 |||||||
 DB 1 ATGGCGGACGATGATGTGATACCCGAGGCGGCGACACAGCGCGGCGGCAAGAG 60

OY 67 CGCTTTGAAGTGAAGAAAGTGAATGCAATGACCCCTGCGGCTGGGATATTTGTTGAT 126
 |||||||
 DB 61 CGCTTTGAAGTGAAGAAAGTGAATGCAATGACCCCTGCGGCTGGGATATTTGTTGAT 120
 |||||||
 OY 127 AACTGGCCATCTGCAAGAACCAATTAATGATTTTCATAGAAATGCAAGTAACCG 186
 |||||||
 DB 121 AACTGGCCATCTGCAAGAACCAATTAATGATTTTCATAGAAATGCAAGTAACCG 180
 |||||||
 OY 187 GCGTCGCTACTCTCAGAAAGTGTACTGTGGATGGGAGTGTAAACCATGCTTTTCAC 246
 |||||||
 DB 181 GCGTCGCTACTCTCAGAAAGTGTACTGTGGATGGGAGTGTAAACCATGCTTTTCAC 240
 |||||||
 OY 247 TTCACCTGATCTCTGCTGCTCAAAACAGACAGAGTGTTCATTGGACAACAGAGAG 306
 |||||||
 DB 241 TTCACCTGATCTCTGCTGCTCAAAACAGACAGAGTGTTCATTGGACAACAGAGAG 300
 |||||||
 OY 307 TGGGAATTCCAAAAGTATGGGCACTAG 333
 |||||||
 DB 301 TGGGAATTCCAAAAGTATGGGCACTAG 327
 |||||||
 RESULT 7
 ID AAA74980 standard; DNA; 504 BP.
 AC AAA74980;
 XX
 DT 02-JAN-2001 (first entry)
 XX
 DE DNA encoding a murine cullin-interacting RING-H2 finger protein (Rbx1).
 XX
 DE Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
 KM tumour suppressor; carcinoma; Ring box associated carcinoma;
 KM von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
 KM cerebellar hemangioblastoma; hemangioma; retinal angiomata;
 KM pheochromocytomas; ss.
 OS Mus sp.
 XX
 PN WO200050445-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 25-FEB-2000; 2000WO-US04838.
 XX
 PR 26-FEB-1999; 99US-0121787.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 PI Conway JA, Conway RC, Kamura T;
 DR MPI: 2000-572067/53.
 XX
 PT Cullin interacting RING-H2 finger protein, a component of von
 PT Hippel-Lindau tumour suppressor complex and Skp1-Cdc53p-F-box protein
 PT (SCF) ubiquitin ligase, useful for diagnosing and treating Ring box
 PT protein associated carcinomas -
 XX
 PS Disclosure; Page 35; 37pp: English.
 XX
 SQ The present sequence encodes a murine cullin-interacting RING-H2 finger
 CC protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide
 CC is a tumour suppressor. Human Rbx1 is useful for diagnosing a
 CC predisposition of a patient to certain carcinomas. It is also useful
 CC for treating Ring box protein associated carcinomas or augmenting
 CC metabolically deficient system in animals. Human Rbx1 is also useful for
 CC evaluating the effectiveness of a therapeutic treatment for Ring box
 CC associated carcinomas. Human Rbx1 can be used to screen for agents which
 CC augment or inhibit the activity of other cullin-containing ubiquitin
 CC ligase and of the VHL (von Hippel-Lindau) complex controlling the
 CC conjugation of ubiquitin or ubiquitin-like proteins to various sets of
 CC target proteins. Carcinomas which may be treated include renal

CC carcinoma, cerebellar hemangioblastomas and hemangiomas, retinal
 CC angiomata and pheochromocytomas.
 XX
 SQ Sequence 504 BP; 117 A; 107 C; 137 G; 143 T; 0 other;

Query Match 63.6%; Score 323; DB 21; Length 504;
 Best Local Similarity 80.6%; Pred. No. 8, 1e-83;
 Matches 394; Conservative 0; Mismatches 85; Indels 10; Gaps 1;

2 CCAAAATGCGCGAGCATGATGTGATACCCCGAGCGACCAACAGCGCGCGGCA 61
 13 CCAAAATGCGCGAGCATGATGTGATACCCCGAGCGACCAACAGCGCGGCA 72
 62 ACAAGGCGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 121
 73 ACAAGGCGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 132
 122 TTGATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 181
 133 TTGATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 192
 182 ACCAGGCGCGCGAGCATGATGTGATACCCCGAGCGACCAACAGCGCGGCA 241
 193 ACCAGGCGCGCGAGCATGATGTGATACCCCGAGCGACCAACAGCGCGGCA 252
 242 TTGATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
 253 TTGATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
 302 GAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
 313 GAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
 362 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
 373 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 422
 422 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
 423 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
 482 GTCAATGA 490
 483 GTAAATGA 491
 Db
 RESULT 8
 AAS86841/c
 ID AAS86841 standard; cDNA; 398 BP.
 XX
 AC AAS86841;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #22645.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.
 DR P-PSDB; ABG22654.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PT
 Claim 1; SEQ ID No 22645; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.

Sequence 398 BP; 122 A; 89 C; 80 G; 107 T; 0 other;
 Query Match 63.2%; Score 321; DB 23; Length 398;
 Best Local Similarity 99.4%; Pred. No. 2.7e-82;
 Matches 343; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

164 GCATGAATGTCACAGGCGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 223
 350 GCATGAATGTCACAGGCGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292
 224 GAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 283
 291 GAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 232
 284 TGTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 343
 231 TGTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 172
 344 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 403
 171 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 113
 404 TTACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 463
 112 TTACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 53
 464 AGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
 52 AGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8
 Db
 RESULT 9
 AAH97860
 ID AAH97860 standard; DNA; 539 BP.
 XX
 AC AAH97860;
 XX
 DT 10-OCT-2001 (first entry)
 XX
 DE Murine 7-transmembrane G-protein coupled receptor coding sequence #104.

XX Murine; hematopoietic stem cell; signalling; vaccine; 7TM-GPCR;
KW 7-transmembrane G-protein coupled protein receptor; ds.
KM
XX
OS Mus sp.
XX WO200160999-A1.
XX
XX
PD 23-AUG-2001.
PP
PA 14-FEB-2001; 2001WO-US04700.
PE 14-FEB-2000; 2000US-0182377.
PX
XX (IMCL-) IMCLONE SYSTEMS INC.
PA (OTPR-) UNIV PRINCETON.
XX
PI Lemischka IR, Witte L, Pereira DS;
XX
XX WPI; 2001-522596/57.
DR
XX DNA Sequences encoding 7-transmembrane G-protein coupled protein
PT receptors characteristic of hematopoietic stem cells, useful for
PT treating leukemia -
PS
XX Claim 1; Page 62; 176pp; English.

CC The present invention relates to murine coding sequences for
CC 7-transmembrane G-protein coupled protein receptors (7TM-GPCRs). The
CC present sequence is one such murine 7TM-GPCR coding sequence. The present
CC sequence was derived from hematopoietic stem cells. The present sequence
CC and its corresponding protein are useful in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate 7TM-GPCR expression.
CC 7TM-GPCRs identify specific signalling molecules, to activate an
CC effector-signalling cascade that triggers an intracellular response and
CC eventually a biological effect.

XQ Sequence 539 BP; 128 A; 112 C; 150 G; 149 T; 0 other;

Query Match	83.0%	Score 319.8	DB 22	Length 539
Best Local Similarity	61.0%	Pred. No. 6.9e-82		
Matches 388	Conservative 0	Mismatches 82	Indels 9	Gaps 1
QY	16	GGGATGATGTGGATATCCCGGAGCGGCACCAACAGCGGCGCGGCAAGAGCGCTTTGAA	75	
Db	1	GGGATGATGTGGATATCCCGGAGCGGCACCAACAGCGGCGGCGGCAAGAGCGCTTTGAA	60	
QY	76	GTGAAAAGTGGAAATGACAGTAGCCCTCTGGGCGTGGGATATTGTGGTGTATTAATGTGCC	135	
Db	61	GTGAAAAGTGGAAATGACAGTAGCCCTCTGGGCGTGGGAGATGTGGTGTATTAATGTGCC	120	
QY	136	ATCTCAGAGAACCATATTATGATATCTTTGATAGAAATGTCAGAGCTAACGAGCGTCCGT	195	
Db	121	ATCTCAGAGAACCATATTATGATATCTTTGATAGAAATGTCAGAGCTAACGAGCGTCCGT	180	
QY	196	ACTTCAGAGAAGTGTACTGTCCGATGGGGAGTCTGTAAACATGCTTTTCACTTCCACTGC	255	
Db	181	ACTTCAGAGAAGTGTACTGTCCGATGGGGAGTCTGTAAACATGCTTTTCACTTCCACTGC	240	
QY	256	ATCTTCGCGTGGCTCAAAAACACGACAGGTGTGTCCATTGGAGACAGAGAGTGGGAATTC	315	
Db	241	ATCTTCGATGGCTCAAAAACGAGGAGGTGTGTCCGTTGGACACAGAGAGTGGGAGTTC	300	
QY	316	CAAAAGTATGGGACATAGGAAAAGACTCTTCATATCAACCTTAATTTGTTGTATATCAT	375	
Db	301	CAGAAATATGGGACATAGGAAAAGACTCTTCGCGAAGGCGTACCCATCTTTTACTGCTCA	360	
QY	376	TTAATTTGACTTTCCCTGCGTTCACCTAATATACAAATTTGGATGGAACGTGTTTTTTCTG	435	
Db	361	GTGA-----CTTCGCTTAATATATATCATTAAGTATACACATGTCCTTTTTCGTTTC	411	
QY	436	CTTTCGTTTTTTCAGTTTGCCTGTTTCTGTAGCCATATTTGATTTCTGTCAAAATTAAGTC	494	

Db	412	CTTTGTTTGGAGTTTGSTGTTCCCGAGGCATATGATTTTGTCGCAATTAAGCC	470
		RESULT 10	
		AAH97862	
		AAH97862 standard; DNA; 586 BP.	
XX		AAH97862;	
XX		10-OCT-2001 (first entry)	
XX		Murine 7-transmembrane G-protein coupled receptor coding sequence #106.	
XX		Murine; hematopoietic stem cell; signalling; vaccine; 7TM-GPCR;	
XX		7-transmembrane G-protein coupled protein receptor; ds.	
XX		Mus sp.	
XX		MO200160999-A1.	
XX		23-AUG-2001.	
XX		14-FEB-2001; 2001WO-US04700.	
XX		14-FEB-2000; 2000US-0182377.	
XX		(IMCL-) IMCLONE SYSTEMS INC.	
XX		(UYPR-) UNIV PRINCETON.	
XX		Lemischka IR, Witte L, Pereira DS;	
XX		WPI; 2001-522596/57.	
XX		DNA Sequences encoding 7-transmembrane G-protein coupled protein	
XX		receptors characteristic of hematopoietic stem cells, useful for	
XX		treating leukemia -	
XX		Claim 1; Page 63; 176pp; English.	
XX		The present invention relates to murine coding sequences for	
XX		7-transmembrane G-protein coupled protein receptors (7TM-GPCRs). The	
XX		present sequence is one such murine 7TM-GPCR coding sequence. The present	
XX		sequence was derived from hematopoietic stem cells. The present sequence	
XX		and its corresponding protein are useful in the prevention, diagnosis and	
XX		treatment of diseases associated with inappropriate 7TM-GPCR expression.	
XX		7TM-GPCRs identify specific signalling molecules, to activate an	
XX		effector-signalling cascade that triggers an intracellular response and	
XX		eventually a biological effect.	
XX		Sequence 586 BP; 140 A; 122 C; 164 G; 159 T; 1 other;	
XX		Query Match 63.0%; Score 319.8; DB 22; Length 586;	
XX		Best Local Similarity 81.0%; Pred. No. 7,1e-82;	
XX		Matches 388; Conservative 0; Mismatches 82; Indels 9; Gaps 1	
Db	16	GGGATGATGTGATATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAGCGCTTTGAA	75
Db	1	GCGATGATGTGATATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAGCGCTTTGAA	60
Db	76	GGAAAAAGTGAATGCACTAGCCCTCTGTGGCCCTGGGATATTGTGTTATACCTGTGCC	135
Db	61	GTTAAAGATGAATGCACTAGCCCTCTGTGGCCCTGGGATATTGTGTTATACCTGTGCC	120
Db	136	ATCTCGAGGAAACACATTTGATCTTTGCAATGATGCAAGCTAACAGGCGTCCGCT	195
Db	121	ATCTCGAGGAAACACATTTGATCTTTGCAATGATGCAAGGCAACAGGCGTCCGCT	180
Db	136	ACTTGAAGAAGTACTGCTGCATGGGAGTCTGTAAACATGCTTTTCACTTCCACTGC	255
Db	181	ATCTCGGAAGATGTACGTTGCTCATGGGAGTCTGGAACATGCTTTTCACTTCCACTGC	240
Db	256	ATCTCTCGTGGCTCAAAACAGCAGAGTGTGTCCATTGGACAACAGAGTGGGAATTG	315

PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234069P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234503P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.

CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 416 BP; 136 A; 83 C; 75 G; 97 T; 25 other;

Query Match 53.3%; Score 271; DB 23; Length 416;
 Best Local Similarity 83.4%; Pred. No. 6.6e-68;
 Matches 363; Conservative 0; Mismatches 0; Indels 72; Gaps 2;

OY 74 AAGTGAAGAAGTGAATGAGTACGAGCCCTGAGGATATGTTGATTAACGTG 133
 DB 416 AAGTGAAGAAGTGAATGAGTACGAGCCCTGAGGATATGTTGATTAACGTG 357
 OY 134 CCATCTGCAGGACCACTTATGATCTTTGCATAGAAATGCAAGCTAACAGGCGTCCG 193
 DB 356 CCATCTGCAGGACCACTTATGATCTTT----- 327
 OY 194 CTACTCAGAAAGTGTACTGTGCGATGGGAGTCTGTACCATGCTTTTCACTTCCACT 253
 DB 326 -----CATGCTTTTCACTTCCACT 308
 OY 254 GCATCTCTCGCTGCTCAAAACACGACAGGTGTTCATTGAGCAACAGAGAGTGGAAAT 313
 DB 307 GCATCTCTCGCTGCTCAAAACACGACAGGTGTTCATTGAGCAACAGAGAGTGGAAAT 248
 OY 314 TCCTAAAGTATGGGACAGTACGAAAGACTTCTTCATCAAGCTTAATGTTGTTATTC 373
 DB 247 TCCTAAAGTATGGGACAGTACGAAAGACTTCTTCATCAAGCTTAATGTTGTTATTC 188
 OY 374 ATTATATGACTTTCCTGCTGTACCTAATTAACAATGATGAGACGTGTTTTTTC 433
 DB 187 ATTATTA-TGACTTTCCTGCTGTACCTAATTAACAATGATGAGACGTGTTTTTTC 129
 OY 434 TGCTTTGTTTTTTCAGTTGCTGTCTGTACCAATATGTTCTGTCAATAAAGT 493
 DB 128 TGCTTTGTTTTTTCAGTTGCTGTCTGTACCAATATGTTCTGTCAATAAAGT 69
 OY 494 CCAGTTGATCTCG 508
 DB 68 CCAGTTGATCTCG 54

Search completed: May 10, 2003, 21:56:21
 Job time : 261 secs

